



-1-

SEQUENCE LISTING

· 110> CURAGEN CORPORATION

RASTELLI, LUKA

· 120> WNT-REGULATED CYTOKINE-LIKE POLYPEPTIDE AND NUCLEIC
ACIDS ENCODING SAME

· 130> 10716/12

· 140> 09/715,418

· 141> 2000-11-16

· 150> 60/166,177

· 151> 1999-11-18

· 160> 48

· 170> PatentIn Ver. 2.1

· 210> 1

· 211> 212

· 212> DNA

· 213> Mus sp.

· 400> 1

gaattcagtg atgttagagag ggcatttag agactcatca agaacttcca taaatactct 60
gtggcggtta aaaagggaaac actgaccctc gctgagcttc gagacctggt tacccagcag 120
ctgccacacc tcatacgag caactgtggg tttagaagaga aaattgccaa cctggcaac 180
tgtaatgact cgaaaactgga gtttggaaagc tt 212

· 210> 2

· 211> 1670

· 212> DNA

· 213> Mus sp.

· 220>

RECEIVED

OCT 11 2001

TECH CENTER 1600/2900

1.221 · modified base

• 222 • (1541)

1223 "n" represents a, t, c, g, other or unknown

400 > 2

tcagggtgagc tggctcctcc atcctgtctc ccagactgcca gcaggtctcc ccctcctcta 60
ggtagatcat gatccatca gatccatcgatccatgtgggcagggctata ggacagacga caaaaactcaa 120
ctcacagaag gaaggaccag tgtaccagga acgatgggac agtgtcggtc agccaatgct 180
gaggatgccc aagaattca gatgttagag agggccattt agacactcat caagaacttc 240
cataaaatact ctgtggcggg taaaaaggaa acactgaccc ctgctgagct tcgagacctg 300
gttaccgc agctgccaca cctcatgccc agcaactgtg gtttagaaga gaaaattgcc 360
aacctggca actgtaatga ctcgaaactg gagtttgaa gcttctggaa gttgattgga 420
gaagcagcca agagtgtgaa gatggagagg cctgttactc ggagctgagg acttctactt 480
ggaacttggtt ggggtgttg gggatagggg agtttttagag gcaactggaaa taaaaccctc 540
aatgtccacc acccccttcc ccagcctgca cctctcctca ttgctgcaat gttcacgttc 600
aggacagggat tccctgtggg ctccatggag ctccctgggtc cagaagtcct catctcaagg 660
gagctcaggg ggtgggttgg ggctggagag gatatgcagg gatcctggaa gggtaaggc 720
caagsaattt ggttagtaggg gaagggcaga aaggaactgg gttatggaa tgatccaaag 780
aycaggatg ggaatctggc tgcatattt gtcctgaaaa gggtgtctga gAACCTACCC 840
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cagstctgcc ccattcctcct tccagtgct gttcctgagt agggcaggg gaaataggag 960
cagagttgca aaagaggctg aggagggcat gacttcatca ctttgggtg agaggaccag 1020
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atgggggtgtt accaaacctt aaccgcctt taggggaaac accccttttgcgcaagtgg 1260
gttaataacg gaagaagccc ggccggatttgccttcacaa gagtcctcccg cggtagatgc 1320
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<210> 3

• 211 • 131

212 PRT

• 213 • Mus sp.

• 400 • 3

Ser Ile Ser Ser Cys Gly Ala Gly Tyr Arg Thr Asp Asp Lys Thr Gln
1 5 10 15

Leu Thr Glu Gly Arg Thr Ser Val Pro Gly Thr Met Gly Gln Cys Arg
20 25 30

Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val Glu Arg Ala
35 40 45

Ile Glu Thr Leu Ile Lys Asn Phe His Lys Tyr Ser Val Ala Gly Lys
50 55 60

Lys Glu Thr Leu Thr Pro Ala Glu Leu Arg Asp Leu Val Thr Gln Gln
65 70 75 80

Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala
85 90 95

Asn Leu Gly Asn Cys Asn Asp Ser Lys Leu Glu Phe Gly Ser Phe Trp
100 105 110

Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Met Glu Arg Pro Val
115 120 125

Thr Arg Ser
130

• 210 • 4

• 211 • 357

• 212 • DNA

• 213 • Homo sapiens

• 220 •

• 221 • modified base

<222> (231)

<223> "n" represents a, t, c, g, other or unknown

<220>

<221> modified base

<222> (337)

<223> "n" represents a, t, c, g, other or unknown

<400> 4

ataggacaac agaactctca ccaaaggacc agacacagtg agcaccatgg gacagtgtcg 60
gtcagccaaac gcagaggatg ctcaggaatt cagtgtatgt gagagggcca ttgagaccct 120
catcaagaac tttcaccagt actccgtgga gggtggaag gagacgctga ccccttctga 180
gtcacgggac ctggtcaccc agcagctgcc ccatctcatg ccgagcaact ntggcctgga 240
agagaaaatt gccaacctgg gcagctgaa tgactctaaa ctggagttca ggagtttctg 300
ggagctgatt ggagaagcgg ccaagagtgt gaagctngag aggactgtcc gggggca 357

<10> 5

<11> 379

<12> DNA

<13> Homo sapiens

<400> 5

gaattccaga gggagttctc agtgcccccg gacaggcctc tccagcttca cactcttggc 60
cgcttctcca atcagctccc agaaaactcct gaactccagt ttagagtcat tgcagctgcc 120
cagggtggca attttctctt ccaggccaca gttgctggc atgagatggg gcagctgctg 180
ggtgaccagg tcccgtagct cagaaggggt cagcgtctcc ttcccacccct ccacggagta 240
atgggtgaaag ttcttgatga gggctcaat ggccctctcc acatcaactga attcctgagc 300
atccctctgcg ttggctgacc gacactgtcc catggtgctc actgtgtctg gtccttttgt 360
gagagttctg ttgtccatat 379

<10> 6

<11> 118

<12> PRT

<13> Homo sapiens

<400> 6

Asp Asn Arg Thr Leu Thr Lys Gly Pro Asp Thr Val Ser Thr Met Gly
1 5 10 15

Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val
20 25 30

Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val
35 40 45

Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val
50 55 60

Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu
65 70 75 80

Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg
85 90 95

Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Leu Glu
100 105 110

Arg Pro Val Arg Gly His
115

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 7

cttgatgagg gtctcaatgg 20

<210> 8

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

<400> 8

ccacatcact gaattcctga gcatcc

26

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

cagacacagt gagcaccatg

20

<210> 10

<211> 98

<212> PRT

<213> Homo sapiens

<400> 10

Met Ala Ala Glu Pro Leu Thr Glu Leu Glu Glu Ser Ile Glu Thr Val

1

5

10

15

Val Thr Thr Phe Phe Thr Phe Ala Arg Gln Glu Gly Arg Lys Asp Ser

20

25

30

Leu Ser Val Asn Glu Phe Lys Glu Leu Val Thr Gln Gln Leu Pro His

35

40

45

Leu Leu Lys Asp Val Gly Ser Leu Asp Glu Lys Met Lys Ser Leu Asp
50 55 60

Val Asn Gln Asp Ser Glu Leu Lys Phe Asn Glu Tyr Trp Arg Leu Ile
65 70 75 80

Gly Glu Leu Ala Lys Glu Ile Arg Lys Lys Lys Asp Leu Lys Ile Arg
85 90 95

Lys Lys

.210> 11

.211> 110

.212> PRT

.213> Homo sapiens

.400> 11

Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile Asn Thr Phe His
1 5 10 15

Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu Asn Gln Gly Glu
20 25 30

Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe Leu Lys Lys Glu
35 40 45

Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu Asp Leu Asp Thr
50 55 60

Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Phe Ile Met Leu Met Ala
65 70 75 80

Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu Gly Asp Glu Gly
85 90 95

Pro Gly His His His Lys Pro Gly Leu Gly Glu Gly Thr Pro

100

105

110

<210> 12

<211> 37

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: 3-100/ICaBP type
calcium binding protein

<400> 12

Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn
1 5 10 15

Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala
20 25 30

Ala Lys Ser Val Lys

35

<210> 13

<211> 37

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: 3-100/ICaBP type
calcium binding protein

<400> 13

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
1 5 10 15

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp
20 25 30

Leu Val Thr Gln Gln

35

<D10> 14

<D11> 19

<D12> PRT

<D13> Unknown Organism

<D20>

<D23> Description of Unknown Organism: Bacterial type II
secretion system protein F

<D00> 14

Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu

1

5

10

15

Glu Lys Ile

<D10> 15

<D11> 10

<D12> PRT

<D13> Unknown Organism

<D20>

<D23> Description of Unknown Organism: Ubiquitin
carboxyl-terminal hydrolases family

<D00> 15

Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser

1

5

10

<D10> 16

<D11> 49

·212· PRT

·213· Unknown Organism

·220·

·223· Description of Unknown Organism: Bacterial
themotaxis sensory transducers protein

·400· 16

Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr
1 5 10 15

Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
20 25 30

Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser
35 40 45

Phe

·210· 17

·211· 32

·212· PRT

·213· Unknown Organism

·220·

·223· Description of Unknown Organism:
Phosphoenolpyruvate carboxykinase (ATP) protein

·400· 17

Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gly Tyr
20 25 30

·210· 18

<211> 33

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Prokaryotic-type
carbonic anhydrases proteins

<400> 18

His Gln Tyr Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu
1 5 10 15

Leu Arg Asp Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn
20 25 30

Cys

<210> 19

<211> 15

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Ergosterol
biosynthesis ERG4/ERG24 family protein

<400> 19

Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg
1 5 10 15

<210> 20

<211> 25

<212> PRT

<213> Unknown Organism

<220>

•223 · Description of Unknown Organism:

Lysosome-associated membrane glycoproteins du

•400 · 20

Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly
1 5 10 15

Ser Cys Asn Asp Ser Lys Ile Glu Phe

20 25

•210 · 21

•211 · 39

•212 · PRT

•213 · Unknown Organism

•220 ·

•223 · Description of Unknown Organism:

Phosphofructokinase proteins

•400 · 21

Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys
1 5 10 15

Asn Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu
20 25 30

Ala Ala Lys Ser Val Lys Leu

35

•210 · 22

•211 · 10

•212 · PRT

•213 · Unknown Organism

•220 ·

•223 · Description of Unknown Organism: PH domain

proteins profile

· 400> 22

Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile
1 5 10

· 210> 23

· 211> 45

· 212> PRT

· 213> Unknown Organism

· 220>

· 223> Description of Unknown Organism: Myotoxins
protein

· 400> 23

Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
1 5 10 15

Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser
20 25 30

Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys
35 40 45

· 210> 24

· 211> 17

· 212> PRT

· 213> Unknown Organism

· 220>

· 223> Description of Unknown Organism:
Phosphatidylinositol-specific phospholipase X

· 400> 24

Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser

1 5 10 15

Cys

· 210 · 25

· 211 · 45

· 212 · PRT

· 213 · Unknown Organism

· 220 ·

· 223 · Description of Unknown Organism: Glypicans
protein

· 400 · 25

Met Gly Gly Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
20 25 30

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu
35 40 45

· 210 · 26

· 211 · 10

· 212 · PRT

· 213 · Unknown Organism

· 220 ·

· 223 · Description of Unknown Organism: Membrane attack
complex components/perforin

· 400 · 26

Ile Lys Asn Phe His Gln Tyr Ser Val Glu
1 5 10

·210· 27

·211· 44

·212· PRT

·213· Unknown Organism

·220·

·223· Description of Unknown Organism: Urease nickel
ligands protein

·400· 27

Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val Glu Gly Gly Lys Glu
1 5 10 15

Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln Leu Pro
20 25 30

His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
35 40

·210· 28

·211· 13

·212· PRT

·213· Unknown Organism

·220·

·223· Description of Unknown Organism: Phosphoglycerate
mutase family phosphohistidi

·400· 28

Gln Glu Phe Ser Asp Val Glu Arg Ala Ile Glu Thr Leu
1 5 10

·210· 29

·211· 10

·212· PRT

·213· Unknown Organism

·220·

·223· Description of Unknown Organism: Ribosomal protein
L23 protein

·400· 29

Glu Leu Arg Asp Leu Val Thr Gln Gln Leu
1 5 10

·210· 30

·211· 41

·212· PRT

·213· Unknown Organism

·220·

·223· Description of Unknown Organism:
2'-5'-oligoadenylate synthetases protein

·400· 30

Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu
1 5 10 15

Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val
20 25 30

Lys Leu Glu Arg Pro Val Arg Gly His
35 40

·210· 31

·211· 24

·212· PRT

·213· Unknown Organism

·220·

·223· Description of Unknown Organism: Formate and

nitrite transporters protein

· 400 · 31

Asp Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly
1 5 10 15

Leu Glu Glu Lys Ile Ala Asn Leu
20

· 210 · 32

· 211 · 34

· 212 · PRT

· 213 · Unknown Organism

· 220 ·

· 223 · Description of Unknown Organism: Glycoprotein
hormones beta chain protein

· 400 · 32

Gln Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp
1 5 10 15

Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser
20 25 30

Val Glu

· 210 · 33

· 211 · 21

· 212 · PRT

· 213 · Unknown Organism

· 220 ·

· 223 · Description of Unknown Organism: Vinculin family
talin-binding region protein

<400> 33

Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln

1

5

10

15

Leu Pro His Leu Met

20

<210> 34

<211> 40

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Beta-lactamases
clas B protein

<400> 34

Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val Glu Gly Gly

1

5

10

15

Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln

20

25

30

Leu Pro His Leu Met Pro Ser Asn

35

40

<210> 35

<211> 21

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Heat shock hsp20
protein family profile

·400· 35

Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser
1 5 10 15

Val Lys Leu Glu Arg

20

·210· 36

·211· 35

·212· PRT

·213· Unknown Organism

·220·

·223· Description of Unknown Organism:

Hydroxymethylglutaryl-coenzyme A lyase protein

·400· 36

Met Gly Gly Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr

20

25

30

Ser Val Glu

35

·210· 37

·211· 294

·212· DNA

·213· Mus sp.

·400· 37

gaatccaga gggagttctc agtgcccccg gacaggcctc tccagcttca cactctggc 60
cgttctcca atcagctccc agaaaactcct gaastccagt ttagagtcat tgcagctgcc 120
caggttggca attttctctt ccaggccaca gttgctcggc atgagatggg gcagctgctg 180
ggtgaccagg tcacgttagct cagaagggtt cagcgcttcc ttcccaccct ccacggagta 240

ctggtaaaat ttcttgatga gggctcaat ggccctctcc acatcactga attc 294

·210· 38

·211· 43

·212· PRT

·213· Homo sapiens

·400· 38

Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser
1 5 10 15

Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu
20 25 30

Val Thr Gln Gln Leu Pro His Leu Met Pro Ser
35 40

·210· 39

·211· 44

·212· PRT

·213· Homo sapiens

·400· 39

Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp
1 5 10 15

Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala
20 25 30

Lys Ser Val Lys Leu Glu Arg Pro Val Arg Gly His
35 40

·210· 40

·211· 44

·212· PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

<400> 40

Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp
1 5 10 15

Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala
20 25 30

Lys Ser Val Lys Leu Glu Arg Pro Val Arg Gly His
35 40

<210> 41

<211> 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: gi/4139958/pdb/1MHO

<400> 41

Glu Lys Ala Val Val Ala Leu Ile Asp Val Phe His Gln Tyr Ser Gly
1 5 10 15

Arg Glu Gly Asp Lys His Lys Leu Lys Lys Ser Glu Leu Lys Glu Leu
20 25 30

Ile Asn Asn Glu Leu Ser His Phe Leu
35 40

<210> 42

<211> 41

>212 > PRT

>213 > Unknown Organism

>220 >

>223 > Description of Unknown Organism: Protein MRP-126

>400 > 42

Glu Lys Ala Ile Asp Val Ile Ile Asp Val Phe His Gln Tyr Ser Arg
1 5 10 15

Arg Glu Gly Asp Lys Asp Thr Leu Thr Arg Lys Glu Leu Lys Leu Leu
20 25 30

Ile Glu Lys Gln Leu Ala Asn Tyr Leu
35 40

>210 > 43

>211 > 41

>212 > PRT

>213 > Unknown Organism

>220 >

>223 > Description of Unknown Organism: ICTACALCIN

>400 > 43

Gln Lys Gly Met Ala Leu Leu Ile Ser Thr Phe His Lys Tyr Ser Gly
1 5 10 15

Lys Glu Gly Asp Lys Cys Thr Leu Thr Lys Gly Glu Leu Lys Asp Leu
20 25 30

Ile Thr Lys Glu Leu Gly Gly Ala Phe
35 40

>210 > 44

>211 > 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: CALGRANULIN B

<400> 44

Glu Ser Ser Ile Glu Thr Ile Ile Asn Ile Phe His Gln Tyr Ser Val
1 5 10 15

Arg Leu Gly His Tyr Asp Thr Leu Ile Gln Lys Glu Phe Lys Gln Leu
20 25 30

Val Gln Lys Glu Leu Pro Asn Phe Leu
35 40

<210> 45

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

<400> 45

Ile Phe His Tyr Ser Gly Leu Glu Leu Leu
1 5 10

<210> 46

<211> 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: CALGRANULIN B

<400> 46

Glu Arg Ser Ile Thr Thr Ile Ile Asp Thr Phe His Gln Tyr Ser Arg
1 5 10 15

Lys Glu Gly His Pro Asp Thr Leu Ser Lys Lys Glu Phe Arg Gln Met
20 25 30

Val Glu Ala Gln Leu Ala Thr Phe Met
35 40

<210> 47

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

<400> 47

Glu Ile Phe His Gln Tyr Ser Gly Leu Glu Leu
1 5 10

<210> 48

<211> 44

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Alignment
sequence

<400> 48

Leu Glu Lys Ala Ile Glu Thr Ile Ile Asn Val Phe His Gln Tyr Ser
1 5 10 15

Gly Arg Glu Gly Asp Lys Asp Thr Leu Ser Lys Lys Glu

20

25

30

Leu Leu Glu Lys Glu Leu Pro Asn Phe Leu Lys Asn

35

40